

10/581773

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SEQUENCE LISTING

<110> Imperial College Innovations Limited  
<120> Therapeutically Useful Molecules  
<130> 28646/42100  
<140> PCT/GB2004/005100  
<141> 2004-12-06  
<150> GB 0328363.7  
<151> 2003-12-06  
<160> 18  
<170> SeqWin99  
<210> 1  
<211> 9  
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<223> Peptide of WT1 which is presented by HLA-A2 class I molecules  
<400> 1  
Arg Met Phe Pro Asn Ala Pro Tyr Leu  
1 5  
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<223> CDR1 of human TCR V -1.5 (V -8.2)  
<400> 2  
Ser Ser Tyr Ser Pro Ser  
1 5  
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<223> CDR2 of human TCR V -1.5 (V -8.2)  
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Tyr Thr Ser Ala Ala Thr Leu  
1 5  
<210> 4  
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<223> CDR3 of human TCR V -1.5 (V -8.2) - 1

<400> 4  
Val Val Ser Pro Phe Ser Gly Gly Ala Asp Gly Leu Thr  
1 5 10

<210> 5  
<211> 12  
<212> PRT  
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<220>  
<223> CDR3 of human TCR V -1.5 (V -8.2) - 2

<400> 5  
Ser Pro Phe Ser Gly Gly Ala Asp Gly Leu Thr  
1 5 10

<210> 6  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> CDR1 of human TCR V -2.1 (V -20.1)

<400> 6  
Asp Phe Gln Ala Thr Thr  
1 5

<210> 7  
<211> 7  
<212> PRT  
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<220>  
<223> CDR2 of human TCR V -2.1 (V -20.1)

<400> 7  
Ser Asn Glu Gly Ser Lys Ala  
1 5

<210> 8  
<211> 8  
<212> PRT  
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<220>  
<223> CDR3 of human TCR V -2.1 (V -20.1) - 1

<400> 8  
Ser Ala Arg Asp Gly Gly Glu Gly  
1 5

<210> 9  
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<212> PRT  
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<220>  
<223> CDR3 of human TCR V -2.1 (V -20.1) - 2

<400> 9  
Arg Asp Gly Gly Glu Gly Ser Glu Thr Gln Tyr  
1 5 10

<210> 10  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Framework amino acid sequence of constant portion C-terminal to CDR3

<400> 10  
Phe Gly Lys Gly Thr His Leu Ile Ile Gln Pro  
1 5 10

<210> 11  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Beginning of constant region of human TCR V -1.5 (V -8.2)

<400> 11  
Tyr Ile Gln Asn Pro  
1 5

<210> 12  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Beginning of framework amino acid sequence of human TCR V -2.1 (V -20.1)

<400> 12  
Ser Glu Thr Gln Tyr  
1 5

<210> 13  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Part of framework amino acid sequence of human TCR V -2.1 (V -20.1)

<400> 13  
Phe Gly Pro Gly Thr Arg Leu Leu Val Leu  
1 5 10

<210> 14  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Part of constant region of human TCR V -2.1 (V -20.1)

<400> 14  
Glu Asp Leu Lys Asn  
1 5

<210> 15

<211> 830  
<212> DNA  
<213> Human TCR V -1.5 (V -8.2)

<400> 15  
atgctcctgc tgctcgccc agtgctcgag gtgattttta ctctggagg aaccagagcc 60  
cagtcggta cccagctga cagccacgtc tctgtctctg aaggaacccc ggtgctgctg 120  
agtgcaact actcatcttc ttattcacca tctcttttctt ggtatgtgca acaccccaac 180  
aaaggactcc agtttctccct gaagtacaca tcagcggcca ccctggtaa aggcatcaac 240  
ggttttgagg ctgaatttaa gaagagtgaa acctccttcc acctgacgaa accctcagcc 300  
catatgagcg acgcggctga gtacttctgt gttgtgagtc cttttcagg aggaggtgct 360  
gacggactca ccttggcaa agggactcat ctaatcatcc agccctatcc cagaaccct 420  
gaccctgccc tgtaccagct gagagactct aaatccagtg acaagtctgt ctgcctattc 480  
accgattttt attctcaaac aaatgtgtca caaagtaagg attctgtatgt gtatatcaca 540  
gacaaaactg tgctagacat gaggtctatg gacttcaaga gcaacagtgc tggtggctgg 600  
agcaaaactt ctgactttgc atgtgcaaac gccttcaaca acagcattat tccagaagac 660  
accttcttcc ccagcccaga aagttcctgt gatgtcaagc tggtcgagaa aagctttgaa 720  
acagatacga acctaactt ctaaaacctg tcagtgattt ggttccaaat cctcctcctg 780  
aaagtggccg ggttaatct gctcatgacg ctggcgctgt ggtccagctg 830

<210> 16  
<211> 276  
<212> PRT  
<213> Human TCR V -1.5 (V -8.2)

<400> 16  
Met Leu Leu Leu Leu Val Pro Val Leu Glu Val Ile Phe Thr Leu Gly  
1 5 10 15  
  
Gly Thr Arg Ala Gln Ser Val Thr Gln Leu Asp Ser His Val Ser Val  
20 25 30  
  
Ser Glu Gly Thr Pro Val Leu Leu Arg Cys Asn Tyr Ser Ser Ser Tyr  
35 40 45  
  
Ser Pro Ser Leu Phe Trp Tyr Val Gln His Pro Asn Lys Gly Leu Gln  
50 55 60  
  
Leu Leu Leu Lys Tyr Thr Ser Ala Ala Thr Leu Val Lys Gly Ile Asn  
65 70 75 80  
  
Gly Phe Glu Ala Glu Phe Lys Lys Ser Glu Thr Ser Phe His Leu Thr  
85 90 95  
  
Lys Pro Ser Ala His Met Ser Asp Ala Ala Glu Tyr Phe Cys Val Val  
100 105 110  
  
Ser Pro Phe Ser Gly Gly Ala Asp Gly Leu Thr Phe Gly Lys Gly  
115 120 125  
  
Thr His Leu Ile Ile Gln Pro Tyr Ile Gln Asn Pro Asp Pro Ala Val  
130 135 140  
  
Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe  
145 150 155 160  
  
Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp  
165 170 175  
  
Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe  
180 185 190  
  
Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys

195	200	205
Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro		
210	215	220
Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu		
225	230	235
Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg		
245	250	255
Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg		
260	265	270
Leu Trp Ser Ser		
275		
<210> 17		
<211> 933		
<212> DNA		
<213> Human TCR V -2.1 (V -20.1)		
<400> 17		
atgctgctgc ttctgctgct tctggggcca ggctccgggc ttgggtgctgt cgtctctcaa	60	
catccgagct gggttatctg taagagtgg aacctctgtga agatcgagtg ccgttccctg	120	
gactttcagg ccacaactat gttttggat cgtcagttcc cgaaaacagag tctcatgctg	180	
atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag	240	
tttctcatca accatgcaag cctgacccctg tccactctga cagtgaccag tgcccatcct	300	
gaagacagca gcttctacat ctgcagtgt agagatgggg gggagggttc ggagacccag	360	
tacttcgggc caggcacgcg gtcctgggt ctcgaggacc taaaaaacgt gttcccaccc	420	
gaggtcgtg tgtttggacc atcagaagca gagatctccc acacccaaaa ggccacactg	480	
gtgtgcgtg ccacaggctt ctaccccgac cacgtggagc tgagctggg ggtgaatggg	540	
aaggagggtgc acagtgggtt cagcacagac ccgcagcccc tcaaggagca gcccgcctc	600	
aatgactcca gatactgcct gagcagccgc ctgagggtct cggccacctt ctggcagaac	660	
cccccgaacc acttccgctg tcaagtccag ttctacgggc tctcggagaa tgacgagtgg	720	
acccaggata gggccaaacc tgcacccag atcgtcagcg ccgaggctg gggtagagca	780	
gactgtggct tcaccccgaa gtcttaccag caaggggtcc tgtctccac catcctctat	840	
gagatcttgc tagggaaaggc caccttgtat gccgtgctgg tcagtcccct cgtgctgatg	900	
gccatggtca agagaaagga ttccagaggc tag	933	
<210> 18		
<211> 310		
<212> PRT		
<213> Human TCR V -2.1 (V -20.1)		
<400> 18		
Met Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala		
1	5	10
		15
Val Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser		
20	25	30
Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe		
35	40	45
Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser		
50	55	60
Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys		
65	70	75
		80
Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr		
85	90	95

Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Arg Asp  
100 105 110

Gly Gly Glu Gly Ser Glu Thr Gln Tyr Phe Gly Pro Gly Thr Arg Leu  
115 120 125

Leu Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val  
130 135 140

Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu  
145 150 155 160

Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp  
165 170 175

Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln  
180 185 190

Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser  
195 200 205

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His  
210 215 220

Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp  
225 230 235 240

Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala  
245 250 255

Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly  
260 265 270

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr  
275 280 285

Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys  
290 295 300

Arg Lys Asp Ser Arg Gly  
305 310